PubMed

National Library of Medicine NLM

NCBI

Entrez   PubMed   Nucleotide   Protein   Genome   Structure   OMIM   PMC   Journals   B

Search | PubMed ▼ | for | Kluyveromyces AND reductase | Preview   Go   Clear

☑ Limits   Preview/Index   History   Clipboard   Details

- Search History will be lost after eight hours of inactivity.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.

Search	Most Recent Queries	Time	Result
#38	Search **Kluyveromyces AND reductase** Field: Title/Abstract	16:15:47	9
#37	Search **Kluyveromyces AND enone** Field: Title/Abstract	16:15:41	0
#36	Search **enone AND reductase** Field: **Title/Abstract**	16:15:28	4
#33	Search **enone reductase** Field: **Title/Abstract**	16:14:28	4
#32	Search **Kluyveromyces AND enzyme AND (enone or ketone or carbon)** Field: Title/Abstract	16:13:50	15
#31	Search **Kluyveromyces AND reductase AND (enone or ketone or carbon)** Field: Title/Abstract	16:13:20	0

Clear History

Jan 29 2004 15:06:34

results of BLAST

BLASTP 2.2.8 [Jan-05-2004]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1076620068-13214-9170067263.BLASTQ3

Query=
                (118 letters)

Database: All non-redundant GenBank CDS
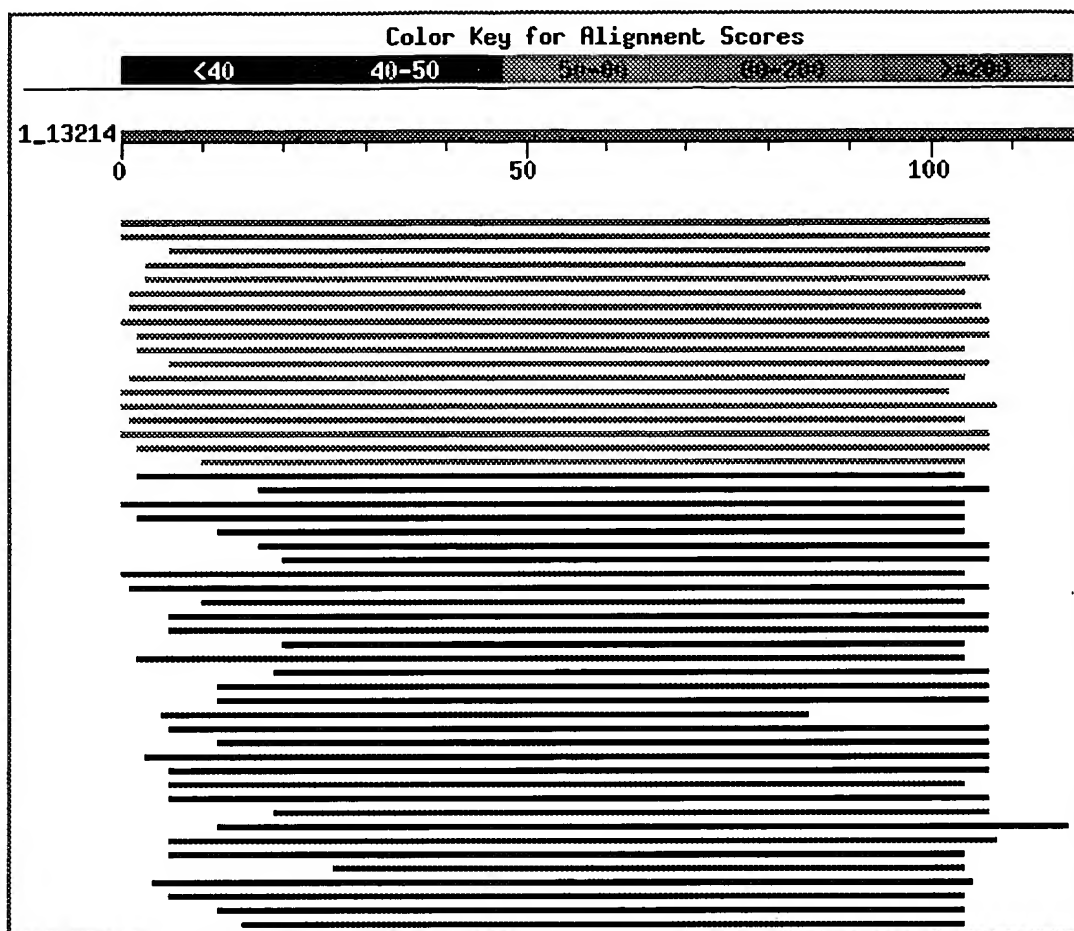translations+PDB+SwissProt+PIR+PRF
                1,643,721 sequences; 539,141,899 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomy reports

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

```
Score    E
Sequences producing significant alignments:                              (bits)  Value

gi|6324195|ref|NP_014265.1|   Ynl134cp [Saccharomyces cerevis...          135     1e-31
gi|6323493|ref|NP_013565.1|   Hypothetical ORF; Ylr460cp [Sac...          134     3e-31
gi|6319945|ref|NP_010026.1|   Hypothetical ORF; Ycr102cp [Sac...          127     4e-29
gi|40741495|gb|EAA60689.1|    hypothetical protein AN8651.2 [A...          96      1e-19
gi|1729996|sp|P54006|TOXD_COCCA  TOXD protein >gi|1027511|em...           77      7e-14
gi|38111915|gb|EAA57410.1|    hypothetical protein MG08380.4 [...          68      3e-11
gi|38111928|gb|EAA57421.1|    hypothetical protein MG08391.4 [...          63      1e-09
gi|38106089|gb|EAA52440.1|    hypothetical protein MG05132.4 [...          61      3e-09
gi|40747879|gb|EAA67031.1|    hypothetical protein AN8409.2 [A...          59      2e-08
gi|38105395|gb|EAA51829.1|    hypothetical protein MG03424.4 [... ·       57      5e-08
```

Alignments

| Get selected sequences | Select all | Deselect all |

```
>gi|6324195|ref|NP_014265.1|   Ynl134cp [Saccharomyces cerevisiae]
gi|1730779|sp|P53912|YNN4_YEAST   HYPOTHETICAL 41.2 KD PROTEIN IN FPR1-TOM22 INTERG
gi|1078063|pir||S55149   hypothetical protein YNL134c - yeast (Saccharomyces cerevi
gi|854503|emb|CAA86891.1|   orf14 [Saccharomyces cerevisiae]
gi|1302076|emb|CAA96016.1|   unnamed protein product [Saccharomyces cerevisiae]
```

```
                    Length = 376

 Score = 135 bits (341), Expect = 1e-31
 Identities = 65/109 (59%), Positives = 82/109 (75%), Gaps = 1/109 (0%)

Query: 1    SVPTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL 60
            S+P T KAV+IE  KAVVK D+ +PEL+EG  L+K  AVAGNPTDWKHI +KIGP+G++L
Sbjct: 4    SIPETMKAVVIENGKAVVKQDIPIPELEEGFVLIKTVAVAGNPTDWKHIDFKIGPQGALL 63


Query: 61   GCDIAGTVVKLGPNA-STDLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
            GCD AG +VKLGPN +    +GD +G +HGAS   P NGAFAEY+ +
Sbjct: 64   GCDAAGQIVKLGPNVDAARFAIGDYIYGVHGASVRFPSNGAFAEYSAI 112
```

☐ >gi|6323493|ref|NP_013565.1| Hypothetical ORF; Ylr460cp [Saccharomyces cerevisi
gi|1730591|sp|P54007|YL60_YEAST   Hypothetical 41.1 kDa protein ON CDC91-PAU4 inter
gi|1363734|pir||S59418   hypothetical protein YLR460c - yeast (Saccharomyces cerevi
gi|717077|gb|AAB64723.1| Ylr460cp [Saccharomyces cerevisiae]

```
                    Length = 376

 Score = 134 bits (337), Expect = 3e-31
 Identities = 65/109 (59%), Positives = 81/109 (74%), Gaps = 1/109 (0%)

Query: 1    SVPTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL 60
            ++P T KAV+IE  KAVVK + +PEL+EG  L+K  AVAGNPTDW HI YKIGP+GSIL
Sbjct: 4    AIPETMKAVVIEDGKAVVKEGIPIPELEEGFVLIKTLAVAGNPTDWAHIDYKIGPQGSIL 63


Query: 61   GCDIAGTVVKLGPNAS-TDLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
            GCD AG +VKLGP  +  D +GD +GF+HG+S   P NGAFAEY+ +
Sbjct: 64   GCDAAGQIVKLGPAVNPKDFSIGDYIYGFIHGSSVRFPSNGAFAEYSAI 112
```

☐ >gi|6319945|ref|NP_010026.1| Hypothetical ORF; Ycr102cp [Saccharomyces cerevisi
gi|140561|sp|P25608|YCZ2_YEAST   40.1 KD PROTEIN IN GIT1-PAU3 INTERGENIC REGION
gi|83274|pir||S19414   hypothetical protein YCR102c - yeast (Saccharomyces cerevisi
gi|1907240|emb|CAA42244.1| hypothetical protein [Saccharomyces cerevisiae]

```
                    Length = 368

 Score = 127 bits (319), Expect = 4e-29
 Identities = 63/103 (61%), Positives = 76/103 (73%), Gaps = 1/103 (0%)

Query: 7    KAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILGCDIAG 66
            KAV+IE  KAVVK V +PEL+EG  L+K  AVAGNPTDW HI YK+GP+GSILGCD AG
Sbjct: 2    KAVVIEDGKAVVKEGVPIPELEEGFVLIKTLAVAGNPTDWAHIDYKVGPQGSILGCDAAG 61


Query: 67   TVVKLGPNAS-TDLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
            +VKLGP    D +GD +GF+HG+S   P NGAFAEY+ +
Sbjct: 62   QIVKLGPAVDPKDFSIGDYIYGFIHGSSVRFPSNGAFAEYSAI 104
```

☐ >gi|40741495|gb|EAA60685.1| hypothetical protein AN8651.2 [Aspergillus nidulans

```
                    Length = 566

 Score = 95.9 bits (237), Expect = 1e-19
 Identities = 52/103 (50%), Positives = 68/103 (66%), Gaps = 2/103 (1%)
```

```
Query: 4    TTQKAVIIEGDK-AVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILGC 62
            +TQKAV+I  K   + TD +P L++   LVK AVA NPTDWKHIAY + P G ++GC
Sbjct: 2    STQKAVVITSPKQGGLVTDRPIPALRDDYILVKNVAVALNPTDWKHIAY-LAPPGVLVGC 60

Query: 63   DIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEY 105
            D AG V ++G N    K GD   GF+HG++Q  P++GAFAEY
Sbjct: 61   DYAGIVEEVGKNVKKPFKKGDRIAGFIHGSNQVQPEDGAFAEY 103
```

☐ >gi|1729996|sp|P54006|TOXD_COCCA   TOXD protein
gi|1027511|emb|CAA63129.1| toxD [Cochliobolus carbonum]
            Length = 297

 Score = 76.6 bits (187), Expect = 7e-14
 Identities = 42/106 (39%), Positives = 62/106 (58%), Gaps = 2/106 (1%)

```
Query: 4    TTQKAVIIEG-DKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILGC 62
            T QKA++ E  +A + +D +P+L++   LV+ +VA NPTDWKHI ++ P G ++GC
Sbjct: 2    TFQKAIVTEAPHRARLVSDRLIPKLRDDYILVRTVSVALNPTDWKHI-LRLSPPGCLVGC 60

Query: 63   DIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
            D AG V ++G +    K GD   GF HG +    +G FAE   V
Sbjct: 61   DYAGIVEEVGRSVKKPFKKGDRVCGFAHGGNAVFSDDGTFAEVITV 106
```

☐ >gi|38111915|gb|EAA57410.1| hypothetical protein MG08380.4 [Magnaporthe grisea ↗
            Length = 353

 Score = 68.2 bits (165), Expect = 3e-11
 Identities = 43/107 (40%), Positives = 66/107 (61%), Gaps = 7/107 (6%)

```
Query: 2    VPTTQKAVIIEGDKAVVKTD--VSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPE-GS 58
            +P+ + A I++ DK +K D   +P+ +    LV+V+AVA NP D H Y+  P  G+
Sbjct: 3    IPSARTA-IVQDDKGGLKIDRNAPMPQPRPNELLVQVKAVAINPCD--HKMYERFPTPGA 59

Query: 59   ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEY 105
            + GCD AG VV+LG + T ++GD   G VHG++ + P++G FAEY
Sbjct: 60   VDGCDFAGIVVQLGSDVKT-FQIGDRVCGAVHGSNPSRPESGTFAEY 105
```

☐ >gi|38111928|gb|EAA57421.1| hypothetical protein MG08391.4 [Magnaporthe grisea ↗
            Length = 400

 Score = 62.8 bits (151), Expect = 1e-09
 Identities = 42/110 (38%), Positives = 59/110 (53%), Gaps = 5/110 (4%)

```
Query: 2    VPTTQKAVIIEGDKAVVKTD--VSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSI 59
            +P++ A+I  D  VK   + +P L+ G LVK AVA NP D+K + +    G+
Sbjct: 46   IPSSHTAIIQHDDAGGVKITPGLPLPVLEPGQVLVKTAAVALNPCDFK-MPQRFSQAGTY 104

Query: 60   LGCDIAGTVVKLGPNASTD--LKVGDTGFGFVHGASQTDPKNGAFAEYAR 107
             GCD AGTVV+L        + LKVGD F   G + D +G+FAEY +
Sbjct: 105  NGCDYAGTVVQLTEEVEKNGLLKVGDRIFAACVGNNPHDKDSGSFAEYLK 154
```

☐ >gi|38106089|gb|EAA52440.1| hypothetical protein MG05132.4 [Magnaporthe grisea ⌐
          Length = 361

 Score = 61.2 bits (147), Expect = 3e-09
 Identities = 42/111 (37%), Positives = 61/111 (54%), Gaps = 7/111 (6%)

Query: 1   SVPTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAY---KIGPEG 57
            ++P+ +A+I   V   V P+L++ LVK AVA NPT+ H +   + P G
Sbjct: 2   AIPSKARALIKTQKGKVEVQTVPTPKLRDNYVLVKTTAVALNPTE-PHAVFDDDTVQP-G 59

Query: 58   SILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
            S++GCD AG VV+ G N+   K GD   G HG + + ++GAFAEY V
Sbjct: 60   SLVGCDFAGVVVEAGDNSR--FKPGDRIAGMAHGGNAENMEDGAFAEYINV 108

☐ >gi|40747875|gb|EAA67031.1| hypothetical protein AN8409.2 [Aspergillus nidulans
          Length = 333

 Score = 58.5 bits (140), Expect = 2e-08
 Identities = 39/108 (36%), Positives = 57/108 (52%), Gaps = 4/108 (3%)

Query: 3   PTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPE-GSILG 61
            P Q A+ I + +   +P L++   LV V+++A NP D K + ++ P G+ LG
Sbjct: 4   PKQQTALKITPEGRIAAVSSPLPSLQDNELLVCVKSIALNPFDAK--SAEMSPTIGATLG 61

Query: 62   CDIAGTVVKLGPNAST-DLKVGDTGFGFVHGASQTDPKNGAFAEYARV 108
            CD AG +V G NA+ + +GD   G V G +   NGAFAEY V
Sbjct: 62   CDFAGKIVATGSNANDFNFSIGDRVCGCVFGNNPNRLDNGAFAEYVAV 109

☐ >gi|38105395|gb|EAA51829.1| hypothetical protein MG03424.4 [Magnaporthe grisea ⌐
          Length = 350

 Score = 57.4 bits (137), Expect = 5e-08
 Identities = 40/104 (38%), Positives = 54/104 (51%), Gaps = 3/104 (2%)

Query: 3   PTTQKAVII-EGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILG 61
            P TQ +++ E D VV+ D P L   LV+V AV NP+D K   P+ +ILG
Sbjct: 6   PATQPGLVVDEHDNVVVRADCPFPSLPADQVLVRVRAVGVNPSDTKMRGPFALPQ-AILG 64

Query: 62   CDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEY 105
            D AG VV +G   D+ VGD G + +P+ GAFA Y
Sbjct: 65   ADFAGDVVAVGAEVR-DVAVGDRVCGAQNELFRPEPERGAFAAY 107

[Get selected sequences] [Select all] [Deselect all]

 Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF
   Posted date: Feb 11, 2004 6:26 AM
 Number of letters in database: 539,141,899
 Number of sequences in database: 1,643,721

```
Lambda      K       H
   0.312    0.134    0.388

Gapped
Lambda      K       H
   0.267    0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 13,287,786
Number of Sequences: 1643721
Number of extensions: 518145
Number of successful extensions: 879
Number of sequences better than 10.0: 30
Number of HSP's better than 10.0 without gapping: 7
Number of HSP's successfully gapped in prelim test: 23
Number of HSP's that attempted gapping in prelim test: 863
Number of HSP's gapped (non-prelim): 31
length of query: 118
length of database: 539,141,899
effective HSP length: 94
effective length of query: 24
effective length of database: 384,632,125
effective search space: 9231171000
effective search space used: 9231171000
T: 11
A: 40
X1: 16 ( 7.2 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (21.8 bits)
S2: 66 (30.0 bits)
```

WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Thursday, February 12, 2004

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR	
☐	L6	alpha-beta-unsaturated adj ketone$2 with (reduc$5 or break or cleav$ or enzym$)	2
☐	L5	alpha-beta-unsaturated adj ketone$2 and nadph	1
☐	L4	alpha-beta-unsaturated adj ketones and nadph	1
☐	L3	alpha-beta-unsaturated ketones and nadph	1917
☐	L2	alpha-beta-unsaturated adj ketones with (reduc$5 or break or cleav$ or enzym$)	2
☐	L1	enone adj reductase	8

END OF SEARCH HISTORY